b) converting the *myo*-2-inosose to 1,2,3,4-tetrahydroxybenzene by acid catalyzed dehydration.

59. (New) The method of claim 58 wherein the first microbe comprises *INO1*.

60. (New) The method of claim 59 wherein the *INO1* gene comprises an *Saccharomyces cerevisiae INO1*.

61. (New) The method of claim 60 wherein *INO1* comprises pAD1.88A.

62. (New) The method of claim 58 wherein the first microbe is an *Escherichia coli*.

63. (New) The method of claim 62 wherein the *Escherichia coli* is JWF1/pAD1.88A.

64. (New) The method of claim 58 wherein the second microbe is *Gluconobacter oxydans*.

65. (New) The method of claim 64 wherein the *Gluconobacter oxydans* is ATCC 621.

66. (New) The method of claim 58 wherein the second microbe comprises a recombinant DNA encoding inositol dehydrogenase.

67. (New) The method of claim 58 wherein the DNA encoding inositol dehydrogenase comprises a *Bacillus subtilis iolG* gene.

68. (New) The method of claim 58 wherein the carbon source comprises glucose.

69. (New) A method for the production of 1,2,3-trihydroxybenzene, comprising producing 1,2,3,4-tetrahydroxybenzene in accordance with claim 1 and reducing the 1,2,3,4-tetrahydroxybenzene to 1,2,3-trihydroxybenzene.

70. (New) A method for the production of 1,2,3,4-tetrahydroxybenzene, comprising:
a) incubating, in the presence of a carbon source, a microbe comprising a first recombinant DNA encoding *myo*-inositol-1-phosphate synthase and a second recombinant DNA encoding inositol dehydrogenase, to produce *myo*-2-inosose; and
b) converting the *myo*-2-inosose to 1,2,3,4-tetrahydroxybenzene by acid catalyzed dehydration.

71. (New) The method of claim 70 wherein the recombinant DNA encoding *myo*-inositol-1-phosphate synthase comprises *INO1*.

72. (New) The method of claim 71 wherein *INO1* comprises a *Saccharomyces cerevisiae INO1*.

73. (New) The method of claim 70 wherein the DNA encoding inositol dehydrogenase comprises *iolG*.

74. (New) The method of claim 70 wherein the DNA encoding inositol dehydrogenase comprises a *Bacillus subtilis iolG*.

75. (New) The method of claim 70 wherein the first recombinant DNA encoding *myo*-inositol-1-phosphate synthase and the second recombinant DNA encoding inositol dehydrogenase comprise pAD2.88A.

76. (New) The method of claim 70 wherein the microbe is an *Escherichia coli*.

77. (New) The method of claim 70 wherein the carbon source comprises glucose.

78. (New) A method for the production of 1,2,3-trihydroxybenzene, comprising producing 1,2,3,4-tetrahydroxybenzene in accordance with claim 70 and reducing the 1,2,3,4-tetrahydroxybenzene to 1,2,3-trihydroxybenzene.

79. (New) A microbe comprising a recombinant DNA encoding *myo*-inositol-1-phosphate synthase.

80. (New) The microbe of claim 79 wherein the recombinant DNA encoding *myo*-inositol-1-phosphate synthase comprises *INO1*.

81. (New) The microbe of claim 80 wherein *INO1* comprises a *Saccharomyces cerevisiae INO1*.

82. (New) The microbe of claim 81 wherein *INO1* comprises pAD1.88A.

83. (New) The microbe of claim 79 which is an *Escherichia coli*.

84. (New) The microbe of claim 83 wherein the *Escherichia coli* is JWF1/pAD1.88A.

85. (New) The microbe of claim 79 further comprising a recombinant DNA encoding inositol dehydrogenase.

86. (New) The microbe of claim 85 wherein the recombinant DNA encoding inositol dehydrogenase comprises a *Bacillus subtilis iolG* gene.

87. (New) A fermentation composition comprising a first microbe which comprises a recombinant DNA encoding *myo*-inositol-1-phosphate synthase and a second microbe which expresses inositol dehydrogenase.

88. (New) The fermentation composition of claim 87 wherein the first microbe comprises an *INO1* gene.

89. (New) The fermentation composition of claim 88 wherein the *INO1* gene comprises a *Saccharomyces cerevisiae INO1* gene.

90. (New) The fermentation composition of claim 89 wherein the *INO1* gene comprises pAD1.88A.

91. (New) The fermentation composition of claim 87 wherein the first microbe is an *Escherichia coli*.

92. (New) The fermentation composition of claim 91 wherein the *Escherichia coli* is JWF1/pAD1.88A.

93. (New) The fermentation composition of claim 87 wherein the second microbe is *Gluconobacter oxydans*.

94. (New) The fermentation composition of claim 93 wherein the *Gluconobacter oxydans* is ATCC 621.

95. (New) The fermentation composition of claim 87 wherein the second microbe comprises a recombinant DNA encoding inositol dehydrogenase.

96. (New) The fermentation composition of claim 95 wherein the DNA encoding inositol dehydrogenase comprises a *Bacillus subtilis iolG* gene.

97. (New) The fermentation composition of claim 87 further comprising glucose.

98. (New) A fermentation composition comprising a microbe which comprises a first recombinant DNA encoding *myo*-inositol-1-phosphate synthase and a second recombinant DNA encoding inositol dehydrogenase.

99. (New) The fermentation composition of claim 98 wherein the recombinant DNA encoding *myo*-inositol-1-phosphate synthase comprises an *INO1* gene.

100. (New) The fermentation composition of claim 99 wherein the *INO1* gene comprises a *Saccharomyces cerevisiae INO1* gene.

101. (New) The fermentation composition of claim 100 wherein the *INO1* gene comprises pAD1.88A.

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102. (New) The fermentation composition of claim 98 wherein the microbe is an *Escherichia coli*.

103. (New) The fermentation composition of claim 98 wherein the DNA encoding inositol dehydrogenase comprises a *Bacillus subtilis iolG* gene.

104. (New) The fermentation composition of claim 98 further comprising glucose.

Remarks

This paper cancels claims 1-57 and adds new claims 58-103 so that claims 58-103 remain pending in the case. No new matter is believed to be added in the amendments to the claims. Support for the new claims can be found in the specification as follows:

Claim 58 finds support in originally filed claim 1. Reference to "incubating, in the presence of a carbon source, a first microbe" finds support at least on page 7, line 25 through page 8, line 2. Reference to a microbe comprising recombinant DNA encoding